

SEQ ID NO: 1

SEQUENCE LENGTH: 1,358

SEQUENCE TYPE: Amino acid

5 TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE OF SEQUENCE

ORGANISM: maize (*Zea mays* L.)

STRAIN: cultivar: Golden Cross Bantam 70

10 SEQUENCE DESCRIPTION

5 10 15  
Met Gly Lys Glu Ala Gly Ala Ala Glu Ser Ser Thr Val Val Leu Ala  
20 25 30  
Val Asn Gly Lys Arg Tyr Glu Ala Ala Gly Val Ala Pro Ser Thr Ser  
15 35 40 45  
Leu Leu Glu Phe Leu Arg Thr Gln Thr Pro Val Arg Gly Pro Lys Leu  
50 55 60  
Gly Cys Gly Glu Gly Gly Cys Gly Ala Cys Val Val Leu Val Ser Lys  
65 70 75 80  
20 Tyr Asp Pro Ala Thr Asp Glu Val Thr Glu Phe Ser Ala Ser Ser Cys  
85 90 95  
Leu Thr Leu Leu His Ser Val Asp Arg Cys Ser Val Thr Thr Ser Glu  
100 105 110  
Gly Ile Gly Asn Thr Arg Asp Gly Tyr His Pro Val Gln Gln Arg Leu  
25 115 120 125

Ser Gly Phe His Ala Ser Gln Cys Gly Phe Cys Thr Pro Gly Met Cys

130

135

140

Met Ser Ile Phe Ser Ala Leu Val Lys Ala Asp Asn Lys Ser Asp Arg

145

150

155

160

5 Pro Asp Pro Pro Ala Gly Phe Ser Lys Ile Thr Thr Ser Glu Ala Glu

165

170

175

Lys Ala Val Ser Gly Asn Leu Cys Arg Cys Thr Gly Tyr Arg Pro Ile

180

185

190

Val Asp Thr Cys Lys Ser Phe Ala Ser Asp Val Asp Leu Glu Asp Leu

10

195

200

205

Gly Leu Asn Cys Phe Trp Lys Lys Gly Glu Glu Pro Ala Glu Val Ser

210

215

220

Arg Leu Pro Gly Tyr Asn Ser Gly Ala Val Cys Thr Phe Pro Glu Phe

225

230

235

240

15 Leu Lys Ser Glu Ile Lys Ser Thr Met Lys Gln Val Asn Asp Val Pro

245

250

255

Ile Ala Ala Ser Gly Asp Gly Trp Tyr His Pro Lys Ser Ile Glu Glu

260

265

270

Leu His Arg Leu Phe Asp Ser Ser Trp Phe Asp Asp Ser Ser Val Lys

20

275

280

285

Ile Val Ala Ser Asn Thr Gly Ser Gly Val Tyr Lys Asp Gln Asp Leu

290

295

300

Tyr Asp Lys Tyr Ile Asp Ile Lys Gly Ile Pro Glu Leu Ser Val Ile

305

310

315

320

25 Asn Lys Asn Asp Lys Ala Ile Glu Leu Gly Ser Val Val Ser Ile Ser

	325	330	335	
	Lys Ala Ile Glu Val Leu Ser Asp Gly Asn Leu Val Phe Arg Lys Ile			
	340	345	350	
	Ala Asp His Leu Asn Lys Val Ala Ser Pro Phe Val Arg Asn Thr Ala			
5	355	360	365	
	Thr Ile Gly Gly Asn Ile Met Met Ala Gln Arg Leu Pro Phe Glu Ser			
	370	375	380	
	Asp Val Ala Thr Val Leu Leu Ala Ala Gly Ser Thr Val Thr Val Gln			
	385	390	395	400
10	Val Ala Ser Lys Arg Leu Cys Phe Thr Leu Glu Glu Phe Leu Glu Gln			
	405	410	415	
	Pro Pro Cys Asp Ser Arg Thr Leu Leu Leu Ser Ile Phe Ile Pro Glu			
	420	425	430	
	Trp Gly Ser Asp Tyr Val Thr Phe Glu Thr Phe Arg Ala Ala Pro Arg			
15	435	440	445	
	Pro Phe Gly Asn Ala Val Ser Tyr Val Asn Ser Ala Phe Leu Ala Arg			
	450	455	460	
	Thr Ser Gly Ser Leu Leu Ile Glu Asp Ile Cys Leu Ala Phe Gly Ala			
	465	470	475	480
20	Tyr Gly Val Asp His Ala Ile Arg Ala Lys Lys Val Glu Asp Phe Leu			
	485	490	495	
	Lys Gly Lys Ser Leu Ser Ser Phe Val Ile Leu Glu Ala Ile Lys Leu			
	500	505	510	
	Leu Lys Asp Thr Val Ser Pro Ser Glu Gly Thr Thr His His Glu Tyr			
25	515	520	525	

Arg Val Ser Leu Ala Val Ser Phe Leu Phe Ser Phe Leu Ser Ser Leu  
 530 535 540  
 Ala Asn Ser Ser Ser Ala Pro Ser Asn Ile Asp Thr Pro Asn Gly Ser  
 545 550 555 560  
 5 Tyr Thr His Glu Thr Gly Ser Asn Val Asp Ser Pro Glu Arg His Ile  
 565 570 575  
 Lys Val Asp Ser Asn Asp Leu Pro Ile Arg Ser Arg Gln Glu Met Val  
 580 585 590  
 Phe Ser Asp Glu Tyr Lys Pro Val Gly Lys Pro Ile Lys Lys Val Gly  
 10 595 600 605  
 Ala Glu Ile Gln Ala Ser Gly Glu Ala Val Tyr Val Asp Asp Ile Pro  
 610 615 620  
 Ala Pro Lys Asp Cys Leu Tyr Gly Ala Phe Ile Tyr Ser Thr His Pro  
 625 630 635 640  
 15 His Ala His Val Arg Ser Ile Asn Phe Lys Ser Ser Leu Ala Ser Gln  
 645 650 655  
 Lys Val Ile Thr Val Ile Thr Ala Lys Asp Ile Pro Ser Gly Gly Glu  
 660 665 670  
 Asn Ile Gly Ser Ser Phe Leu Met Gln Gly Glu Ala Leu Phe Ala Asp  
 20 675 680 685  
 Pro Ile Ala Glu Phe Ala Gly Gln Asn Ile Gly Val Val Ile Ala Glu  
 690 695 700  
 Thr Gln Arg Tyr Ala Asn Met Ala Ala Lys Gln Ala Val Val Glu Tyr  
 705 710 715 720  
 25 Ser Thr Glu Asn Leu Gln Pro Pro Ile Leu Thr Ile Glu Asp Ala Ile

725 730 735  
 Gln Arg Asn Ser Tyr Ile Gln Ile Pro Pro Phe Leu Ala Pro Lys Pro  
 740 745 750  
 Val Gly Asp Tyr Asn Lys Gly Met Ala Glu Ala Asp His Lys Ile Leu  
 5 755 760 765  
 Ser Ala Glu Val Lys Leu Glu Ser Gln Tyr Tyr Phe Tyr Met Glu Thr  
 770 775 780  
 Gln Ala Ala Leu Ala Ile Pro Asp Glu Asp Asn Cys Ile Thr Ile Tyr  
 785 790 795 800  
 10 Ser Ser Thr Gln Met Pro Glu Leu Thr Gln Asn Leu Ile Ala Arg Cys  
 805 810 815  
 Leu Gly Ile Pro Phe His Asn Val Arg Val Ile Ser Arg Arg Val Gly  
 820 825 830  
 Gly Gly Phe Gly Gly Lys Ala Met Lys Ala Thr His Thr Ala Cys Ala  
 15 835 840 845  
 Cys Ala Leu Ala Ala Phe Lys Leu Arg Arg Pro Val Arg Met Tyr Leu  
 850 855 860  
 Asp Arg Lys Thr Asp Met Ile Met Ala Gly Gly Arg His Pro Met Lys  
 865 870 875 880  
 20 Ala Lys Tyr Ser Val Gly Phe Lys Ser Asp Gly Lys Ile Thr Ala Leu  
 885 890 895  
 His Leu Asp Leu Gly Ile Asn Ala Gly Ile Ser Pro Asp Val Ser Pro  
 900 905 910  
 Leu Met Pro Arg Ala Ile Ile Gly Ala Leu Lys Lys Tyr Asn Trp Gly  
 25 915 920 925

Thr Leu Glu Phe Asp Thr Lys Val Cys Lys Thr Asn Val Ser Ser Lys

930

935

940

Ser Ala Met Arg Ala Pro Gly Asp Val Gln Gly Ser Phe Ile Ala Glu

945

950

955

960

5 Ala Ile Ile Glu His Val Ala Ser Ala Leu Ala Leu Asp Thr Asn Thr

965

970

975

Val Arg Arg Lys Asn Leu His Asp Phe Glu Ser Leu Glu Val Phe Tyr

980

985

990

Gly Glu Ser Ala Gly Glu Ala Ser Thr Tyr Ser Leu Val Ser Met Phe

10

995

1000

1005

Asp Lys Leu Ala Leu Ser Pro Glu Tyr Gln His Arg Ala Ala Met Ile

1010

1015

1020

Glu Gln Phe Asn Ser Ser Asn Lys Trp Lys Lys Arg Gly Ile Ser Cys

1025

1030

1035

1040

15

Val Pro Ala Thr Tyr Glu Val Asn Leu Arg Pro Thr Pro Gly Lys Val

1045

1050

1055

Ser Ile Met Asn Asp Gly Ser Ile Ala Val Glu Val Gly Gly Ile Glu

1060

1065

1070

Ile Gly Gln Gly Leu Trp Thr Lys Val Lys Gln Met Thr Ala Phe Gly

20

1075

1080

1085

Leu Gly Gln Leu Cys Pro Asp Gly Gly Glu Cys Leu Leu Asp Lys Val

1090

1095

1100

Arg Val Ile Gln Ala Asp Thr Leu Ser Leu Ile Gln Gly Gly Met Thr

1105

1110

1115

1120

25

Ala Gly Ser Thr Thr Ser Glu Thr Ser Cys Glu Thr Val Arg Gln Ser

	1125	1130	1135	
	Cys Val Ala Leu Val Glu Lys Leu Asn Pro Ile Lys Glu Ser Leu Glu			
	1140	1145	1150	
	Ala Lys Ser Asn Thr Val Glu Trp Ser Ala Leu Ile Ala Gln Ala Ser			
5	1155	1160	1165	
	Met Ala Ser Val Asn Leu Ser Ala Gln Pro Tyr Trp Thr Pro Asp Pro			
	1170	1175	1180	
	Ser Phe Lys Ser Tyr Leu Asn Tyr Gly Ala Gly Thr Ser Glu Val Glu			
	1185	1190	1195	1200
10	Val Asp Ile Leu Thr Gly Ala Thr Thr Ile Leu Arg Ser Asp Leu Val			
	1205	1210	1215	
	Tyr Asp Cys Gly Gln Ser Leu Asn Pro Ala Val Asp Leu Gly Gln Ile			
	1220	1225	1230	
	Glu Gly Cys Phe Val Gln Gly Ile Gly Phe Phe Thr Asn Glu Asp Tyr			
15	1235	1240	1245	
	Lys Thr Asn Ser Asp Gly Leu Val Ile His Asp Gly Thr Trp Thr Tyr			
	1250	1255	1260	
	Lys Ile Pro Thr Val Asp Asn Ile Pro Lys Glu Phe Asn Val Glu Met			
	1265	1270	1275	1280
20	Phe Asn Ser Ala Pro Asp Lys Lys Arg Val Leu Ser Ser Lys Ala Ser			
	1285	1290	1295	
	Gly Glu Pro Pro Leu Val Leu Ala Thr Ser Val His Cys Ala Met Arg			
	1300	1305	1310	
	Glu Ala Ile Arg Ala Ala Arg Lys Glu Phe Ser Val Ser Thr Ser Pro			
25	1315	1320	1325	



SEQ ID NO: 2

SEQUENCE LENGTH: 4,412

SEQUENCE TYPE: Nucleic acid

5 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE OF SEQUENCE

ORGANISM: maize (*Zea mays* L.)

10 STRAIN: cultivar: Golden Cross Bantam 70

FEATURES OF SEQUENCE:

KEY: CDS

LOCATION: 46..4120 (including termination codon)

IDENTIFICATION METHOD: E

15 SEQUENCE DESCRIPTION

GTG CTG TGT TGT GCT GTG CTG CGT GCT GTG GAG GGG GAG GAG GAG ATG 48

GGG AAG GAG GCA GGG GCA GCG GAG TCG TCG ACG GTG GTG CTG GCC GTC 96

AAC GGC AAG CGC TAC GAG GCG GCC GGC GTG GCT CCG TCC ACG TCG CTG 144

CTG GAG TTC CTC CGC ACC CAG ACG CCC GTC AGA GGC CCC AAG CTC GGC 192

20 TGC GGC GAA GGT GGC TGC GGT GCA TGC GTG GTC CTC GTC TCC AAG TAC 240

GAC CCG GCC ACG GAC GAG GTG ACC GAG TTC TCT GCC AGC TCC TGC CTG 288

ACG CTG CTC CAC AGC GTG GAC CGC TGC TCA GTG ACC ACC AGC GAG GGA 336

ATC GGC AAC ACC AGG GAT GGC TAC CAC CCC GTG CAG CAG CGC CTC TCC 384

GGC TTC CAC GCC TCG CAG TGC GGC TTC TGC ACA CCC GGC ATG TGC ATG 432

25 TCC ATC TTC TCC GCC CTT GTC AAG GCC GAC AAC AAG TCC GAT CGC CCG 480

	GAC CCT CCT GCT GGC TTC TCC AAG ATC ACT ACC TCG GAG GCA GAG AAG	528
	GCT GTC TCG GGC AAC CTT TGT CGT TGC ACC GGA TAC AGA CCC ATT GTT	576
	GAC ACC TGC AAA AGC TTT GCC TCT GAT GTT GAC CTC GAG GAC CTA GGC	624
	CTC AAC TGT TTC TGG AAG AAG GGC GAA GAA CCT GCA GAA GTC AGC AGG	672
5	CTG CCG GGG TAC AAC AGC GGT GCC GTC TGC ACC TTT CCA GAG TTT CTC	720
	AAA TCC GAA ATC AAG TCT ACT ATG AAG CAG GTG AAC GAT GTC CCC ATT	768
	GCA GCC TCA GGT GAT GGC TGG TAC CAT CCT AAG AGC ATT GAA GAG CTT	816
	CAC AGG TTG TTT GAT TCC AGC TGG TTT GAT GAC AGT TCT GTG AAG ATT	864
	GTT GCT TCA AAC ACT GGG TCT GGA GTG TAC AAG GAT CAG GAC CTC TAC	912
10	GAC AAG TAC ATT GAC ATC AAA GGA ATC CCA GAG CTT TCA GTC ATC AAT	960
	AAA AAC GAC AAA GCA ATT GAG CTT GGA TCA GTT GTG TCC ATC TCT AAA	1008
	GCT ATT GAA GTG CTG TCA GAT GGA AAT TTG GTC TTC AGA AAG ATT GCT	1056
	GAT CAC CTC AAC AAA GTG GCT TCA CCG TTT GTT CGG AAC ACT GCA ACC	1104
	ATA GGA GGA AAC ATA ATG ATG GCA CAA AGG TTG CCA TTT GAA TCG GAT	1152
15	GTT GCA ACC GTG CTC CTA GCT GCG GGT TCG ACA GTC ACA GTC CAG GTG	1200
	GCT TCC AAA AGG CTG TGC TTC ACT CTG GAG GAA TTC TTG GAA CAA CCT	1248
	CCA TGT GAT TCT AGG ACC CTG CTG CTG AGC ATA TTT ATC CCA GAA TGG	1296
	GGT TCA GAC TAT GTC ACC TTT GAG ACT TTC CGA GCC GCC CCA CGA CCA	1344
	TTT GGA AAT GCT GTC TCT TAT GTA AAC TCT GCT TTC TTG GCA AGG ACA	1392
20	TCA GGC AGC CTT CTA ATT GAG GAT ATA TGC TTG GCA TTT GGT GCC TAC	1440
	GGA GTC GAT CAT GCC ATC AGA GCT AAG AAG GTT GAA GAT TTC TTG AAG	1488
	GGA AAA TCG CTG AGC TCA TTT GTG ATA CTT GAA GCA ATT AAA CTA CTC	1536
	AAA GAT ACC GTT TCA CCA TCA GAA GGC ACT ACA CAT CAT GAA TAC AGG	1584
	GTC AGC TTG GCT GTC AGT TTC TTG TTC AGT TTC TTA TCT TCC CTT GCC	1632
25	AAC AGT TCG AGT GCA CCA TCA AAT ATT GAT ACT CCC AAT GGG TCA TAT	1680

	ACT CAT GAA ACT GGT AGC AAT GTG GAC TCA CCT GAG AGG CAT ATT AAG	1728
	GTT GAC AGC AAT GAT TTG CCA ATT CGT TCA AGA CAA GAA ATG GTT TTC	1776
	AGC GAT GAG TAC AAG CCT GTT GGC AAG CCG ATC AAG AAA GTC GGG GCA	1824
	GAG ATC CAA GCA TCA GGG GAG GCT GTG TAC GTT GAT GAT ATC CCT GCT	1872
5	CCC AAG GAT TGC CTC TAT GGA GCA TTT ATC TAC AGC ACA CAT CCT CAT	1920
	GCT CAT GTG AGA AGT ATC AAC TTC AAA TCA TCC TTG GCT TCA CAG AAG	1968
	GTC ATC ACA GTT ATA ACC GCA AAG GAT ATT CCA AGC GGT GGA GAA AAT	2016
	ATT GGA AGC AGC TTC CTG ATG CAA GGA GAA GCA CTA TTT GCA GAT CCA	2064
	ATC GCT GAA TTT GCT GGT CAA AAT ATT GGT GTC GTG ATT GCT GAA ACA	2112
10	CAA AGA TAT GCT AAT ATG GCT GCA AAG CAA GCT GTT GTT GAG TAT AGC	2160
	ACA GAA AAT CTG CAG CCA CCA ATT CTG ACA ATA GAA GAT GCC ATC CAA	2208
	AGA AAC AGC TAC ATC CAA ATT CCC CCA TTT TTA GCT CCA AAG CCA GTT	2256
	GGT GAC TAC AAC AAA GGG ATG GCT GAA GCA GAC CAC AAG ATT CTA TCA	2304
	GCA GAG GTA AAA CTT GAA TCC CAG TAC TAC TTC TAC ATG GAA ACT CAA	2352
15	GCA GCA CTA GCG ATT CCT GAT GAA GAT AAC TGC ATA ACA ATC TAT TCC	2400
	TCG ACA CAA ATG CCT GAG CTC ACA CAA AAT TTG ATA GCA AGG TGT CTT	2448
	GGC ATT CCA TTT CAC AAT GTC CGT GTC ATC AGC AGA AGA GTA GGA GGA	2496
	GGC TTT GGT GGA AAG GCA ATG AAA GCA ACG CAT ACT GCA TGT GCA TGT	2544
	GCC CTT GCT GCC TTC AAG CTG CGG CGT CCA GTT AGG ATG TAC CTC GAT	2592
20	CGC AAG ACG GAC ATG ATA ATG GCT GGA GGG AGA CAT CCA ATG AAG GCG	2640
	AAG TAC TCT GTT GGG TTC AAG TCA GAT GGC AAG ATC ACA GCC TTG CAC	2688
	CTA GAT CTT GGA ATC AAT GCT GGA ATA TCA CCA GAT GTG AGT CCA TTG	2736
	ATG CCA CGT GCT ATC ATA GGA GCT CTC AAA AAG TAC AAC TGG GGC ACT	2784
	CTT GAA TTT GAC ACC AAG GTC TGC AAG ACA AAT GTC TCA TCA AAG TCA	2832
25	GCA ATG CGA GCT CCT GGA GAT GTG CAG GGC TCT TTC ATC GCT GAA GCC	2880

	ATC ATC GAG CAT GTT GCC TCA GCA CTC GCA CTA GAC ACT AAC ACC GTC	2928
	AGG AGG AAG AAC CTT CAT GAT TTT GAA AGC CTT GAA GTT TTC TAT GGA	2976
	GAA AGT GCA GGT GAA GCT TCT ACA TAC AGC CTG GTT TCC ATG TTT GAC	3024
	AAG CTG GCC TTG TCT CCA GAA TAC CAG CAC AGG GCT GCA ATG ATT GAG	3072
5	CAG TTC AAT AGC AGC AAC AAA TGG AAG AAA CGC GGC ATT TCT TGT GTG	3120
	CCA GCC ACT TAT GAG GTT AAT CTT CGA CCA ACT CCA GGC AAG GTG TCA	3168
	ATC ATG AAT GAT GGT TCC ATC GCT GTC GAG GTT GGA GGA ATT GAG ATA	3216
	GGT CAA GGA TTG TGG ACT AAA GTG AAG CAG ATG ACG GCC TTT GGA CTG	3264
	GGA CAG CTG TGT CCT GAT GGT GGC GAA TGC CTT CTG GAC AAG GTT CGG	3312
10	GTT ATC CAG GCA GAC ACA TTA AGC CTG ATC CAA GGA GGT ATG ACT GCT	3360
	GGG AGC ACC ACT TCT GAA ACT AGC TGT GAA ACA GTT CGG CAA TCT TGT	3408
	GTT GCA CTG GTT GAG AAG CTG AAC CCT ATC AAG GAG AGT CTC GAA GCT	3456
	AAG TCC AAC ACA GTG GAA TGG AGT GCC TTG ATT GCT CAG GCA AGC ATG	3504
	GCG AGT GTG AAC CTA TCA GCA CAG CCG TAC TGG ACT CCT GAT CCA TCT	3552
15	TTC AAG AGC TAC TTG AAC TAC GGA GCT GGC ACC AGT GAG GTG GAA GTT	3600
	GAT ATC CTA ACA GGA GCA ACC ACA ATT CTG CGA AGC GAC CTG GTG TAT	3648
	GAC TGC GGG CAG AGC CTA AAC CCT GCT GTA GAC TTG GGC CAG ATC GAG	3696
	GGC TGC TTT GTC CAA GGA ATA GGG TTC TTC ACG AAC GAG GAC TAC AAG	3744
	ACG AAT TCC GAC GGG TTG GTC ATC CAC GAC GGC ACA TGG ACG TAC AAG	3792
20	ATC CCC ACG GTG GAT AAT ATC CCG AAG GAG TTC AAT GTT GAG ATG TTT	3840
	AAC AGC GCC CCT GAC AAG AAG CGT GTC CTA TCT TCC AAA GCG TCG GGC	3888
	GAG CCG CCG CTG GTT CTC GCA ACC TCG GTG CAC TGC GCG ATG AGG GAG	3936
	GCC ATC AGG GCG GCG AGG AAG GAG TTC TCG GTC AGC ACC AGC CCC GCG	3984
	AAA TCC GCC GTC ACA TTC CAG ATG GAC GTG CCG GCG ACG ATG CCT GTC	4032
25	GTC AAG GAG CTC TGC GGC CTC GAC GTC GTG GAG AGG TAC CTC GAG AAC	4080

	GTG	TCT	GCC	GCC	AGT	GCC	GGC	CCA	AAC	ACA	GCG	AAA	GCA	TAG	ATC	CAG	4128
	CAG	GCC	TCA	GGG	TGC	AGT	CGG	CGC	ACT	GCC	AGA	GAT	GAT	GTG	TGC	TGC	4176
	CCT	GAT	GTA	CAG	ACA	GTA	CAG	TAC	AGA	GGA	GAG	AGA	ATT	GGG	GGA	ACT	4224
	CAG	GAA	CTG	CGA	GGA	GCG	ATG	AAC	AGT	ATA	TAG	AGT	GAA	AAA	TAA	AAG	4272
5	TGC	TTC	GTA	CTA	ATA	ATC	ACT	AGA	AAA	AAT	TAT	GCA	CAT	CTC	CCA	CGC	4320
	ACT	ACC	GGC	ACG	ACT	GTT	GAA	TAT	TTT	GTA	AAA	TAA	GAT	GTC	ATA	AGC	4368
	TAT	TTA	TTT	TCT	GTA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AA		4412

[illegible]

SEQ ID NO: 3

SEQUENCE LENGTH: 1,349

SEQUENCE TYPE: Amino acid

5 TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE OF SEQUENCE

ORGANISM: maize (*Zea mays* L.)

STRAIN: cultivar: Golden Cross Bantam 70

10 SEQUENCE DESCRIPTION

5 10 15  
Met Glu Met Gly Lys Ala Ala Ala Val Val Leu Ala Val Asn Gly Lys  
20 25 30  
Arg Tyr Glu Ala Ala Gly Val Asp Pro Ser Thr Thr Leu Leu Glu Phe  
15 35 40 45  
Leu Arg Thr His Thr Pro Val Arg Gly Pro Lys Leu Gly Cys Gly Glu  
50 55 60  
Gly Gly Cys Gly Ala Cys Val Val Leu Val Ser Lys Tyr Asp Pro Ala  
65 70 75 80  
20 Thr Asp Glu Val Thr Glu Phe Ser Ala Ser Ser Cys Leu Thr Leu Leu  
85 90 95  
His Ser Val Asp Arg Cys Ser Val Thr Thr Ser Glu Gly Ile Gly Asn  
100 105 110  
Thr Lys Asp Gly Tyr His Pro Val Gln Gln Arg Leu Ser Gly Phe His  
25 115 120 125

Ala Ser Gln Cys Gly Phe Cys Thr Pro Gly Met Cys Met Ser Ile Phe

130

135

140

Ser Ala Leu Val Lys Ala Asp Lys Ala Ala Asn Arg Pro Ala Pro Pro

145

150

155

160

5 Ala Gly Phe Ser Lys Leu Thr Ser Ser Glu Ala Glu Lys Ala Val Ser

165

170

175

Gly Asn Leu Cys Arg Cys Thr Gly Tyr Arg Pro Ile Val Asp Ala Cys

180

185

190

Lys Ser Phe Ala Ala Asp Val Asp Leu Glu Asp Leu Gly Leu Asn Cys

10

195

200

205

Phe Trp Lys Lys Gly Asp Glu Pro Ala Asp Val Ser Lys Leu Pro Gly

210

215

220

Tyr Asn Ser Gly Asp Val Cys Thr Phe Pro Asp Phe Leu Lys Ser Glu

225

230

235

240

15 Met Lys Ser Ser Ile Gln Gln Ala Asn Ser Ala Pro Val Pro Val Ser

245

250

255

Asp Asp Gly Trp Tyr Arg Pro Arg Ser Ile Asp Glu Leu His Arg Leu

260

265

270

Phe Gln Ser Ser Ser Phe Asp Glu Asn Ser Val Lys Ile Val Ala Ser

20

275

280

285

Asn Thr Gly Ser Gly Val Tyr Lys Asp Gln Asp Leu Tyr Asp Lys Tyr

290

295

300

Ile Asp Ile Lys Gly Ile Pro Glu Leu Ser Val Ile Asn Arg Asn Asp

305

310

315

320

25 Lys Gly Ile Glu Leu Gly Ser Val Val Ser Ile Ser Lys Ala Ile Glu

325 330 335  
 Val Leu Ser Asp Gly Asn Leu Val Phe Arg Lys Ile Ala Gly His Leu  
 340 345 350  
 Asn Lys Val Ala Ser Pro Phe Val Arg Asn Thr Ala Thr Ile Gly Gly  
 5 355 360 365  
 Asn Ile Val Met Ala Gln Arg Leu Pro Phe Ala Ser Asp Ile Ala Thr  
 370 375 380  
 Ile Leu Leu Ala Ala Gly Ser Thr Val Thr Ile Gln Val Ala Ser Lys  
 385 390 395 400  
 10 Arg Leu Cys Phe Thr Leu Glu Glu Phe Leu Gln Gln Pro Pro Cys Asp  
 405 410 415  
 Ser Arg Thr Leu Leu Leu Ser Ile Phe Ile Pro Glu Trp Gly Ser Asn  
 420 425 430  
 Asp Val Thr Phe Glu Thr Phe Arg Ala Ala Pro Arg Pro Leu Gly Asn  
 15 435 440 445  
 Ala Val Ser Tyr Val Asn Ser Ala Phe Leu Ala Arg Thr Ser Leu Asp  
 450 455 460  
 Ala Ala Ser Lys Asp His Leu Ile Glu Asp Ile Cys Leu Ala Phe Gly  
 465 470 475 480  
 20 Ala Tyr Gly Ala Asp His Ala Ile Arg Ala Arg Lys Val Glu Asp Tyr  
 485 490 495  
 Leu Lys Gly Lys Thr Val Ser Ser Ser Val Ile Leu Glu Ala Val Arg  
 500 505 510  
 Leu Leu Lys Gly Ser Ile Lys Pro Ser Glu Gly Ser Thr His Pro Glu  
 25 515 520 525

	Tyr	Arg	Ile	Ser	Leu	Ala	Val	Ser	Phe	Leu	Phe	Thr	Phe	Leu	Ser	Ser
	530							535								540
	Leu	Ala	Asn	Ser	Leu	Asn	Glu	Ser	Ala	Lys	Val	Ser	Gly	Thr	Asn	Glu
	545					550						555				560
5	His	Ser	Pro	Glu	Lys	Gln	Leu	Lys	Leu	Asp	Ile	Asn	Asp	Leu	Pro	Ile
						565					570					575
	Arg	Ser	Arg	Gln	Glu	Ile	Phe	Phe	Thr	Asp	Ala	Tyr	Lys	Pro	Val	Gly
						580					585					590
	Lys	Ala	Ile	Lys	Lys	Ala	Gly	Val	Glu	Ile	Gln	Ala	Ser	Gly	Glu	Ala
10						595					600					605
	Val	Tyr	Val	Asp	Asp	Ile	Pro	Ala	Pro	Lys	Asp	Cys	Leu	Tyr	Gly	Ala
						610					615					620
	Phe	Ile	Tyr	Ser	Thr	His	Pro	His	Ala	His	Val	Lys	Ser	Ile	Asn	Phe
	625					630						635				640
15	Lys	Pro	Ser	Leu	Ala	Ser	Gln	Lys	Ile	Ile	Thr	Val	Ile	Thr	Ala	Lys
						645						650				655
	Asp	Ile	Pro	Ser	Gly	Gly	Gln	Asn	Val	Gly	Tyr	Ser	Phe	Pro	Met	Ile
						660						665				670
	Gly	Glu	Glu	Ala	Leu	Phe	Ala	Asp	Pro	Val	Ala	Glu	Phe	Ala	Gly	Gln
20						675										685
	Asn	Ile	Gly	Val	Val	Ile	Ala	Gln	Thr	Gln	Lys	Tyr	Ala	Tyr	Met	Ala
						690						695				700
	Ala	Lys	Gln	Ala	Ile	Ile	Glu	Tyr	Ser	Thr	Glu	Asn	Leu	Gln	Pro	Pro
	705						710					715				720
25	Ile	Leu	Thr	Ile	Glu	Asp	Ala	Ile	Glu	Arg	Ser	Ser	Phe	Phe	Gln	Thr

		725		730		735										
	Leu	Pro	Phe	Val	Ala	Pro	Lys	Pro	Val	Gly	Asp	Tyr	Asp	Lys	Gly	Met
				740					745						750	
	Ser	Glu	Ala	Asp	His	Lys	Ile	Leu	Ser	Ala	Glu	Val	Lys	Ile	Glu	Ser
5			755					760							765	
	Gln	Tyr	Phe	Phe	Tyr	Met	Glu	Pro	Gln	Val	Ala	Leu	Ala	Ile	Pro	Asp
			770					775						780		
	Glu	Asp	Asn	Cys	Ile	Thr	Ile	Tyr	Phe	Ser	Thr	Gln	Leu	Pro	Glu	Ser
	785				790					795						800
10	Thr	Gln	Asn	Val	Val	Ala	Lys	Cys	Val	Gly	Ile	Pro	Phe	His	Asn	Val
				805						810					815	
	Arg	Val	Ile	Thr	Arg	Arg	Val	Gly	Gly	Gly	Phe	Gly	Gly	Lys	Ala	Leu
				820					825					830		
	Lys	Ser	Met	His	Val	Ala	Cys	Ala	Cys	Ala	Val	Ala	Ala	Leu	Lys	Leu
15			835					840						845		
	Gln	Arg	Pro	Val	Arg	Met	Tyr	Leu	Asp	Arg	Lys	Thr	Asp	Met	Ile	Met
			850					855						860		
	Ala	Gly	Gly	Arg	His	Pro	Met	Lys	Val	Lys	Tyr	Ser	Val	Gly	Phe	Lys
	865				870					875						880
20	Ser	Asn	Gly	Lys	Ile	Thr	Ala	Leu	His	Leu	Asp	Leu	Gly	Ile	Asn	Gly
				885						890					895	
	Gly	Ile	Ser	Pro	Asp	Met	Ser	Pro	Met	Ile	Ala	Ala	Pro	Val	Ile	Gly
				900					905						910	
	Ser	Leu	Lys	Lys	Tyr	Asn	Trp	Gly	Asn	Leu	Ala	Phe	Asp	Thr	Lys	Val
25			915					920						925		

Cys Lys Thr Asn Val Ser Ser Lys Ser Ser Met Arg Ala Pro Gly Asp

930

935

940

Ala Gln Gly Ser Phe Ile Ala Glu Ala Ile Ile Glu His Val Ala Ser

945

950

955

960

5 Ala Leu Ser Ala Asp Thr Asn Thr Ile Arg Arg Lys Asn Leu His Asp

965

970

975

Phe Glu Ser Leu Ala Val Phe Phe Gly Asp Ser Ala Gly Glu Ala Ser

980

985

990

Thr Tyr Ser Leu Val Thr Met Phe Asp Lys Leu Ala Ser Ser Pro Glu

10

995

1000

1005

Tyr Gln His Arg Ala Glu Met Val Glu Gln Phe Asn Arg Ser Asn Lys

1010

1015

1020

Trp Lys Lys Arg Gly Ile Ser Cys Val Pro Val Thr Tyr Glu Val Gln

1025

1030

1035

1040

15 Leu Arg Pro Thr Pro Gly Lys Val Ser Ile Met Asn Asp Gly Ser Ile

1045

1050

1055

Ala Val Glu Val Gly Gly Val Glu Leu Gly Gln Gly Leu Trp Thr Lys

1060

1065

1070

Val Lys Gln Met Thr Ala Phe Gly Leu Gly Gln Leu Cys Pro Gly Gly

20

1075

1080

1085

Gly Glu Ser Leu Leu Asp Lys Val Arg Val Ile Gln Ala Asp Thr Leu

1090

1095

1100

Ser Met Ile Gln Gly Gly Val Thr Gly Gly Ser Thr Thr Ser Glu Thr

1105

1110

1115

1120

25 Ser Cys Glu Ala Val Arg Lys Ser Cys Val Ala Leu Val Glu Ser Leu

	1125	1130	1135
	Lys Pro Ile Lys Glu Asn Leu Glu Ala Lys Thr Gly Thr Val Glu Trp		
	1140	1145	1150
	Ser Ala Leu Ile Ala Gln Ala Ser Met Ala Ser Val Asn Leu Ser Ala		
5	1155	1160	1165
	His Ala Tyr Trp Thr Pro Asp Pro Thr Phe Thr Ser Tyr Leu Asn Tyr		
	1170	1175	1180
	Gly Ala Gly Thr Ser Glu Val Glu Ile Asp Val Leu Thr Gly Ala Thr		
	1185	1190	1195
			1200
10	Thr Ile Leu Arg Ser Asp Leu Val Tyr Asp Cys Gly Gln Ser Leu Asn		
	1205	1210	1215
	Pro Ala Val Asp Leu Gly Gln Val Glu Gly Ala Phe Val Gln Gly Val		
	1220	1225	1230
	Gly Phe Phe Thr Asn Glu Glu Tyr Ala Thr Asn Ser Asp Gly Leu Val		
15	1235	1240	1245
	Ile His Asp Gly Thr Trp Thr Tyr Lys Ile Pro Thr Val Asp Thr Ile		
	1250	1255	1260
	Pro Lys Gln Phe Asn Val Glu Leu Ile Asn Ser Ala Arg Asp Gln Lys		
	1265	1270	1275
			1280
20	Arg Val Leu Ser Ser Lys Ala Ser Gly Glu Pro Pro Leu Leu Leu Ala		
	1285	1290	1295
	Ser Ser Val His Cys Ala Met Arg Glu Ala Ile Arg Ala Ala Arg Lys		
	1300	1305	1310
	Glu Phe Ser Val Cys Thr Gly Pro Ala Asn Ser Ala Ile Thr Phe Gln		
25	1315	1320	1325

Met Asp Val Pro Ala Thr Met Pro Val Val Lys Glu Leu Cys Gly Leu

1330

1335

1340

Asp Val Val Glu Arg Tyr Leu Glu Ser Val Ser Ala Ala Ser Pro Thr

1345

5 Asn Thr Ala Lys Ala

0291344-100397

SEQ ID NO: 4

SEQUENCE LENGTH: 4,359

SEQUENCE TYPE: Nucleic acid

5 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE OF SEQUENCE

ORGANISM: maize (*Zea mays L.*)

10 STRAIN: cultivar: Golden Cross Bantam 70

FEATURES OF SEQUENCE:

KEY: CDS

LOCATION: 91..4138 (including termination codon)

IDENTIFICATION METHOD: E

15 SEQUENCE DESCRIPTION

CCG GCT CTC TCG GTG CAG ACG TCC GGG ACT AGT ACG TGG ATC GGG CCG	48
GGG GCA ACT CGA GTC GTC AAG AAG GCT GCT ACC TGC TAG AGG ATG GAG	96
ATG GGG AAG GCG GCG GCG GTG GTG CTG GCG GTG AAC GGC AAG CGG TAC	144
GAG GCC GCC GGC GTG GAC CCG TCG ACG ACG CTG CTG GAG TTC CTG CGC	192
20 ACC CAC ACG CCC GTC AGG GGG CCC AAG CTC GGC TGC GGC GAA GGT GGC	240
TGC GGT GCA TGC GTT GTG CTT GTC TCG AAG TAC GAC CCA GCC ACC GAC	288
GAG GTG ACC GAG TTC TCA GCG AGC TCC TGC CTG ACG CTG CTC CAT AGC	336
GTG GAC CGC TGC TCG GTG ACC ACC AGC GAG GGC ATT GGC AAC ACC AAG	384
GAT GGC TAC CAC CCT GTG CAG CAG CGC CTC TCC GGC TTC CAC GCC TCC	432
25 CAG TGC GGT TTC TGC ACG CCC GGC ATG TGC ATG TCC ATC TTC TCT GCG	480

CTT GTC AAA GCC GAC AAG GCG GCC AAC CGG CCA GCC CCA CCG GCC GGC 528

TTC TCC AAG CTC ACT TCC TCG GAG GCT GAG AAG GCT GTC TCT GGC AAC 576

CTG TGC CGC TGC ACA GGG TAC AGG CCC ATC GTC GAC GCC TGT AAG AGC 624

TTC GCA GCC GAT GTT GAT CTT GAG GAC CTG GGC CTC AAC TGC TTC TGG 672

5 AAG AAG GGT GAT GAG CCT GCA GAT GTC AGC AAG CTG CCA GGC TAC AAC 720

AGT GGT GAC GTC TGC ACT TTC CCT GAC TTT CTC AAA TCT GAG ATG AAG 768

TCC TCA ATT CAG CAG GCT AAC AGC GCT CCA GTT CCT GTT TCT GAC GAC 816

GGC TGG TAC CGT CCT AGG AGC ATT GAC GAG CTT CAC AGG TTG TTT CAA 864

TCT AGC TCC TTC GAT GAA AAT TCC GTG AAG ATA GTG GCT TCA AAC ACT 912

10 GGG TCT GGA GTG TAC AAG GAT CAG GAC CTT TAT GAC AAG TAC ATT GAC 960

ATC AAA GGA ATC CCA GAG CTT TCA GTC ATC AAC AGA AAC GAC AAA GGA 1008

ATT GAG CTT GGA TCA GTT GTG TCC ATC TCT AAA GCT ATT GAG GTG CTG 1056

TCA GAT GGA AAT CTC GTC TTC AGA AAG ATT GCT GGT CAC CTG AAC AAA 1104

GTG GCT TCA CCG TTT GTT CGG AAC ACT GCA ACC ATA GGT GGA AAC ATA 1152

15 GTC ATG GCA CAA AGA TTG CCA TTC GCA TCG GAC ATT GCA ACC ATA CTA 1200

CTA GCT GCA GGT TCA ACA GTC ACA ATC CAG GTG GCT TCC AAA AGG CTG 1248

TGC TTC ACT CTG GAG GAG TTC TTG CAG CAG CCT CCA TGC GAT TCT AGG 1296

ACC CTG CTG CTG AGC ATA TTT ATC CCG GAA TGG GGC TCA AAT GAT GTC 1344

ACC TTT GAG ACT TTC CGA GCA GCA CCT CGT CCA CTT GGC AAT GCT GTC 1392

20 TCA TAT GTC AAT TCA GCT TTC TTG GCA AGG ACT TCA TTG GAT GCA GCA 1440

TCA AAG GAC CAT CTC ATC GAG GAT ATA TGT CTG GCG TTC GGT GCT TAT 1488

GGA GCT GAT CAT GCT ATT AGA GCT AGA AAG GTT GAG GAT TAC CTG AAG 1536

GGC AAA ACA GTG AGC TCG TCT GTC ATA CTT GAA GCT GTT CGG TTG CTT 1584

AAA GGG TCT ATT AAA CCA TCA GAA GGC TCA ACA CAT CCT GAG TAT AGA 1632

25 ATT AGC TTG GCT GTC AGT TTC TTG TTT ACC TTC CTA TCC TCC CTT GCC 1680

AAC AGC TTG AAT GAA TCT GCA AAG GTT AGT GGT ACC AAC GAG CAC TCA 1728  
CCA GAG AAG CAA CTC AAG TTG GAC ATC AAT GAT TTG CCA ATA CGA TCA 1776  
AGA CAA GAA ATA TTT TTC ACT GAT GCA TAT AAG CCA GTT GGC AAA GCA 1824  
ATT AAG AAA GCT GGG GTA GAG ATC CAA GCT TCA GGG GAA GCT GTG TAC 1872  
5 GTT GAT GAT ATC CCT GCT CCC AAA GAT TGC CTC TAT GGG GCA TTT ATT 1920  
TAT AGC ACA CAC CCT CAT GCA CAT GTA AAG TCA ATC AAC TTT AAA CCA 1968  
TCT TTG GCT TCA CAG AAG ATC ATC ACA GTT ATC ACT GCA AAG GAT ATT 2016  
CCC AGC GGT GGA CAA AAT GTT GGT TAT AGC TTC CCG ATG ATT GGA GAA 2064  
GAA GCA CTT TTT GCA GAT CCA GTT GCT GAA TTT GCT GGT CAA AAT ATT 2112  
10 GGT GTC GTG ATT GCT CAA ACA CAG AAG TAT GCC TAC ATG GCG GCA AAG 2160  
CAA GCC ATC ATT GAG TAT AGC ACA GAA AAT CTG CAG CCA CCA ATT CTG 2208  
ACA ATA GAA GAT GCA ATT GAA CGA AGC AGC TTC TTC CAA ACC CTC CCA 2256  
TTT GTA GCT CCT AAG CCA GTT GGT GAT TAC GAC AAA GGG ATG TCT GAA 2304  
GCT GAT CAC AAG ATT TTA TCG GCA GAG GTA AAA ATT GAA TCC CAA TAC 2352  
15 TTT TTC TAC ATG GAG CCA CAA GTG GCG CTA GCT ATT CCT GAT GAA GAT 2400  
AAC TGC ATA ACC ATC TAT TTT TCG ACA CAA TTA CCT GAG TCC ACA CAA 2448  
AAT GTG GTT GCA AAG TGC GTT GGC ATT CCA TTT CAC AAT GTC CGT GTA 2496  
ATC ACC AGA AGG GTC GGA GGA GGC TTT GGT GGA AAA GCA TTG AAA TCA 2544  
ATG CAT GTT GCA TGT GCA TGT GCA GTT GCT GCA TTG AAG CTA CAA CGT 2592  
20 CCA GTT CGG ATG TAC CTC GAT CGC AAG ACA GAC ATG ATA ATG GCA GGC 2640  
GGG CGG CAT CCT ATG AAG GTG AAG TAC TCT GTT GGG TTC AAG TCA AAC 2688  
GGC AAG ATC ACA GCC TTA CAT CTT GAT CTT GGG ATC AAT GGT GGA ATA 2736  
TCT CCA GAT ATG AGT CCA ATG ATT GCA GCA CCT GTC ATA GGT TCT CTC 2784  
AAA AAG TAC AAC TGG GGC AAT CTT GCA TTT GAC ACC AAG GTC TGC AAA 2832  
25 ACA AAT GTC TCA TCA AAA TCG TCA ATG AGA GCT CCT GGA GAT GCG CAG 2880

GGC TCT TTC ATT GCT GAA GCC ATC ATC GAG CAT GTT GCC TCG GCA CTT 2928  
TCA GCC GAC ACT AAT ACC ATA AGG AGA AAG AAC CTT CAT GAC TTT GAG 2976  
AGC CTT GCA GTG TTC TTT GGA GAT AGT GCA GGT GAA GCT TCT ACA TAC 3024  
AGC CTT GTC ACC ATG TTC GAT AAA TTG GCC TCC TCT CCA GAA TAC CAG 3072  
5 CAC CGA GCT GAA ATG GTG GAA CAA TTC AAC CGA AGC AAC AAG TGG AAG 3120  
AAG CGT GGC ATT TCT TGT GTG CCT GTA ACA TAT GAG GTG CAG CTT CGG 3168  
CCA ACT CCA GGA AAG GTG TCT ATC ATG AAT GAT GGT TCC ATT GCT GTT 3216  
GAG GTT GGA GGG GTT GAG CTA GGC CAA GGG TTG TGG ACA AAA GTG AAG 3264  
CAG ATG ACG GCA TTC GGA CTA GGA CAG CTG TGT CCT GGC GGC GGT GAA 3312  
10 AGC CTT CTA GAC AAG GTG CGG GTC ATC CAG GCC GAC ACA TTG AGC ATG 3360  
ATC CAA GGA GGG GTC ACT GGT GGG AGC ACC ACT TCT GAA ACT AGC TGT 3408  
GAA GCA GTT CGT AAG TCG TGT GTT GCA CTC GTC GAG AGC TTG AAG CCA 3456  
ATC AAG GAG AAT CTG GAG GCT AAA ACT GGC ACA GTG GAA TGG AGT GCC 3504  
TTG ATT GCA CAG GCA AGT ATG GCG AGC GTT AAC TTA TCG GCA CAT GCA 3552  
15 TAC TGG ACC CCT GAT CCA ACT TTC ACA AGC TAT TTG AAC TAC GGA GCC 3600  
GGC ACT AGC GAG GTG GAA ATT GAT GTC CTG ACA GGA GCA ACA ACA ATT 3648  
CTA AGG AGT GAC CTT GTC TAC GAT TGC GGG CAA AGC TTG AAC CCT GCT 3696  
GTC GAT TTG GGG CAG GTG GAA GGT GCA TTC GTA CAA GGA GTA GGC TTC 3744  
TTC ACA AAC GAG GAG TAC GCA ACC AAC TCT GAC GGG TTG GTC ATC CAC 3792  
20 GAT GGC ACA TGG ACG TAC AAG ATC CCC ACG GTC GAC ACC ATC CCA AAG 3840  
CAG TTC AAC GTT GAG CTG ATC AAC AGC GCC CGT GAC CAG AAG CGC GTC 3888  
CTC TCT TCC AAA GCA TCG GGC GAG CCT CCG CTT CTC CTA GCT TCC TCT 3936  
GTG CAC TGC GCA ATG AGG GAG GCC ATC AGG GCC GCC AGG AAA GAA TTC 3984  
TCG GTC TGC ACT GGT CCA GCG AAC TCC GCC ATC ACG TTC CAG ATG GAC 4032  
25 GTG CCG GCA ACG ATG CCT GTC GTC AAG GAG CTC TGC GGC CTG GAT GTC 4080

